MicroRNA profiling reveals two distinct p53-related human pluripotent stem cell states.

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Public Summary:
Reprogramming methodologies have provided multiple routes for achieving pluripotency. However, pluripotency is generally considered to be an almost singular state, with subtle differences described between induced pluripotent stem cells (iPSCs) and embryonic stem cells (ESCs). Here we show that this is not the case. Differences between pluripotent cell types are important considerations when developing a therapy. We profiled micro RNA expression levels across 49 human cell lines, including ESCs, iPSCs, differentiated cells, and cancer cell lines. MicroRNAs are short RNAs that regulated gene expression in important ways. We found that the resulting miRNA profiles divided the iPSCs and hESCs examined into two distinct categories irrespective of the cell line origin. The miRNAs that defined these two pluripotency categories also distinguished cancer cells from differentiated cells. Transcriptome analysis suggested that several gene sets related to p53 - an important protein involved in suppression of tumor progression - distinguished these categories, and overexpression of the p53-targeting miRNAs miR-92 and miR-141 in iPSCs was sufficient to change their classification status. Thus, our results suggest a subdivision of pluripotent stem cell states that is independent of their origin but related to p53 network status.

Scientific Abstract:
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